

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 18, 2002, 02:09:56 ; Search time 8718.72 Seconds
(without alignments)
1893.746 Million cell updates/sec

Title: US-09-719-748-1_COPY_98_886

Perfect score: 789
Sequence: 1 tatgacatcgagagagagct.....ctctcagacacccttgatc 789

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*

- 1: gb_da:*
- 2: gb_hlg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pac:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vl:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
- 20: em_om:*
- 21: em_or:*
- 22: em_ov:*
- 23: em_pat:*
- 24: em_ph:*
- 25: em_pl:*
- 26: em_ro:*
- 27: em_sts:*
- 28: em_un:*
- 29: em_vl:*
- 30: em_hlg_hum:*
- 31: em_hlg_inv:*
- 32: em_hlg_other:*
- 33: em_hlgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	787.4	99.8	1742	9	AF052941 Homo sapi
2	784.2	99.4	1739	9	AB018001 Homo sapi
3	697.8	88.4	1883	10	BC022165 Mus muscu
4	693	87.8	1757	10	AB018002 Mus muscu
5	569.6	72.2	1474	10	AF052942 Mus muscu
6	495.2	62.8	2055	9	AB022341 Homo sapi
7	494.6	62.7	1410	10	AB007143 Mus muscu
8	494.6	62.7	1429	6	AR076190 Sequence
9	494.6	62.7	1429	6	AR124103 Sequence
10	493.6	62.7	1429	6	E23385 DNA encodin
11	493.6	62.6	2105	9	AB007144 Homo sapi
12	493.6	62.6	2132	6	AR076189 Sequence
13	493.6	62.6	2132	6	AR124102 Sequence
14	493.6	62.6	2132	6	E23384 DNA encodin
15	493.6	62.6	2224	6	BD004888 Novel gen
16	493.6	62.6	2224	9	AK027590 Homo sapi
17	480.2	60.9	1514	10	AR069711 Rattus no
18	469	59.4	5345	19	MDAPK
19	445	56.4	1590	9	BC003614 Homo sapi
20	443.4	56.2	5910	9	HSDAPK
21	398.2	50.5	4935	6	AR080622 Sequence
22	398.2	50.5	5886	6	AR121934 Sequence
23	319.8	40.5	4918	10	BC021490 Mus muscu
24	244.6	31.0	132817	2	AC034201 Homo sapi
25	244.6	31.0	210617	2	AC034201 Homo sapi
26	239.4	30.3	247196	2	AC073822 Mus muscu
27	222.4	28.2	194028	9	AC021541 Homo sapi
28	208.6	26.4	3983	4	S57131
29	207	26.2	2960	9	AB056801 Macaca fa
30	203.8	25.8	1317	4	S80867
31	202.2	25.6	1415	9	HSWYOLCKI
32	202.2	25.6	3181	9	AB037663 Homo sapi
33	202.2	25.6	5719	9	AF069601 Homo sapi
34	202.2	25.6	5926	6	AX329738 Sequence
35	202.2	25.6	5926	6	AX330278 Sequence
36	202.2	25.6	5926	6	AX333040 Sequence
37	202.2	25.6	5926	6	AX337264 Sequence
38	202.2	25.6	5926	6	HSU48959 Homo sapien
39	197.6	25.0	1366	3	ACTWIRCH
40	197.4	25.0	3426	9	HSNICK
41	195.2	24.7	101222	2	AC103501 Rattus no
42	193.6	24.5	480	6	AR119795 Sequence
43	193.6	24.5	480	6	AR126755 Sequence
44	193.6	24.5	480	6	AR128915 Sequence
45	193.6	24.5	480	6	AR130846 Sequence

ALIGNMENTS

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source Location/Qualifiers
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/organism="Homo sapiens"
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/tissue-type="kidney"
32..1144
/note="protein serine/threonine kinase"
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/db_xref="GI:3560543"
/translation="MFQASMRSPNMEPFKQKQVDFYDIGEELSGOPAIYKCKREKS
TGLEYAKFIKKROSRSRKSRETEIREVSIIRQVLAHVITLHDVYENTDVVLI
LEIVSGEELDFPLAKESLSEEAATSFIKQILDGNVNIYHTKIAFDLAKPENIMLDK
NIPPIPHIKLIDFGLAHEIDEGVERFNITGTFEVAPELVNPELSEADMSIGVITY
ILLSGASPLFDITKQETLANITAVSYNDEEFQSTSLADFIKLLVKEKRLUTI
QEARLHPWITPVDMQAMRVRESVNIENPEFKQYVRWRKLSFISVLCNHLTRSLMK
KVHLRPEDILNCSDETDIEDIARRKALHPRRSST5"
misc_feature
923..1021
/note="calcium/calmodulin binding region; binding site"
BASE COUNT 441 a 437 c 504 g 360 t
ORIGIN

Query Match 99.8%; Score 787.4; DB 9; Length 1742;
Best Local Similarity 99.9%; Pred. No. 1.4e-172;
Matches 788; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tatgacatcgagaggaagctggagagtgccagttgcacatcgtygaagaatgcccggag 60
DB 98 TATGACATCGAGAGGAGACTGGGAGTGGCCAGTTGCCATCGTGAAGAAGTCCGGAG 157

QY 61 aagagcaggggcttgagatgacagccaaatcatcaagaagcggcagagccggcgagc 120
DB 158 AAGAGCAGGGGCTTGATGATGCAAGCCAAATTCAACAAGACGCGGCGAGC 217

QY 121 cggcgagggtgagccgggaagagatcgagcgggaggtgaaatccctcgcggaagtgctg 180
DB 218 CGGCGAGGCTGAGCCCGGAGAGATCGAGCGGAGTGAGACATCTCGCGAGGTGCTG 277

QY 181 caccacaatgcatcagctcagcagctctatgagaacccgacccgaagtggtgacatc 240
DB 278 CACCAATGTCATCACCTGACAGCTCTATGAGAACCCACGACGAGTGGTCTCATC 337

QY 241 cttagcagtgatgctgagaggaagctctcgatctcctcgccagaagaagatcagtgagt 300
DB 338 CTTGAGCTAGTGTCTGGAGGAGAGCTCTTGCATTTCCGCGCCAGAAAGAGTCACTAGT 397

QY 301 gagagagagagccacacagctcatcaagcagatcctgagtggtgagtaacctcaaca 360
DB 398 GAGAGAGGAGCCACACGCTTATTAAAGCAGATCCGTGATGGGGTGMACTACCTTCACACA 457

QY 361 aagaaaattgctcacttgatcctcaagccaaaacatcatgctgttgagaagaataatt 420
DB 458 AAGAAAATTGCTCATTGATCTCAAGCCAGAAAACATTATGTTGTTAGACAGAATATT 517

QY 421 cccattccacacatcaagctgtagtacttgctgctggtcgcacgaataatgagaatgagtt 480
DB 518 CCCATTCCACACATCAAGCTGATTGACTTGTGCTGCGCTCAAGAAATGGAAGATGAGATT 577

QY 481 gaatttaagaataattttggagacggcggaatttgctgtctccagaataatgtgaaactagag 540
DB 578 GAAATTTAAGAAATATTTTGGAGCCCGGAATTTGTTGCTCCAGAAATGTGAACATACGAG 637

QY 541 cccctggagctcgagagctgagacatgtagagcaatggcgtcatcacactataatcctctaagt 600
DB 638 CCCCTGGGCTCTGGAGGCTGACATGTGAGAGCATTAAGCGTCACTACCTTACTTTAAGT 697

QY 601 ggaagcattcccttctctgagagacagaaagcaggaataaacatgycaaatatcacatcaatg 660
DB 698 GGAGCATCCCTTCTCTGAGAGACAGAAAGCAAGAAACATGGAATAATCATCACTAATG 757

QY 661 agttaagacttgatgaggaattcttcaagcatacgagcagagctggccaagaacttaatt 720

DB 758 ACTIACGACTTGATGAGCAATTTCTACGCATACGAGGAGCTGGCCAAAGCACTTATT 817

QY 721 cggagagctctgtttaaagagccgggaagcgctacaatccaagaagctctcaagac 780
DB 818 CGGAAGCTTGTGTTAAAGAGACCGGAACGGCTCACAATCCAGAAGGCTCTCAGACAC 877

QY 781 cccctgagatc 789
DB 878 CCTGTGATC 886

RESULT 2
AB018001 1739 bp mRNA linear pri 04-DEC-1999
LOCUS AB018001
DEFINITION Homo sapiens mRNA for Death-associated protein kinase 2, complete cds.
ACCESSION AB018001
VERSION AB018001.1 GI:6521209
KEYWORDS Death-associated protein kinase 2.
SOURCE Homo sapiens CDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
Kawai,T., Nomura,F., Hoshino,K., Copeland,N.G., Gilbert,D.J.,
Jenkins,N.A. and Akira,S.
Death-associated protein kinase 2 is a new
calcium/calmodulin-dependent protein kinase that signals apoptosis
through its catalytic activity
Oncogene 18 (23), 3471-3480 (1999)
99303018
2 (bases 1 to 1739)
Akira,S. and Kawai,T.
Direct Submission
Submitted (28-SEP-1998) Shizuo Akira, Hyogo College of Medicine,
Department of Biochemistry, Mukogawa-cho 1-1, Nishinomiya, Hyogo
663-8501, Japan (E-mail:akira@hyo-med.ac.jp, Tel:81-798-45-6357,
Fax:81-798-46-3164)

FEATURES
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1739
polyA_site
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BASE COUNT 439 a 439 c 504 g 357 t
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Query Match 99.4%; Score 784.2; DB 9; Length 1739;
Best Local Similarity 99.6%; Pred. No. 7.6e-172;
Matches 786; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tatgacatcgagaggaagctggagagtgccagttgcacatcgtygaagaatgcccggag 60
DB 97 TATGACATCGAGAGGAGACTGGGAGTGGCCAGTTGCCATCGTGAAGAAGTCCGGAG 156

QY 61 aagagcaggggcttgagatgacagccaaatcatcaagaagcggcagagccggcgagc 120

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Db 157 AAGAGCAGGGGCTTGATGATGACAGCAAGTTCATCAAGAGGGGACAGCCGGGAGC 216
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Qy 121 cggcggtgtgtgagccggagagagatcgagcggagaggtgagcattcctgcgaggtgtc 180
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Db 217 CGCCGGGTGTGTGAGCCGGGGAGATCGAGCCGGAGTGCATCTCTGCGGAGGTCTG 276
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Qy 181 caccacaatgtcatcagctgcagcagcgtctatagagaccgacgagcgtgtgtgacatc 240
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Db 277 CACCAAAATGTCTACACGCTGCACGACGCTTATGAGAACCGCACCGAGTGTGCTCATC 326
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Qy 241 ctgagctagtgctgtagagagagccttcgattcctggtccgagagagagtagcagat 300
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Db 337 CTGAGCTAGTGTCTGAGAGAGAGCTCTTGATTTCTGCTGCGCAGAAAGAGTCACTGAGT 396
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Qy 301 gagagagagccacagctcatcaatgaagcagatccctgtgaggttgaactcctcacaca 360
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Db 397 GAGGAGAGGCCACAGCTTCATTAAAGCAATCTGGATGGGTGAACCTTCACTTCACACA 456
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Qy 361 aagaaatgtctcacttgatctcacaagccagaaacatatagtttatagaagaagaatatt 420
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Db 457 AAGAAAATGCTCATCTTTGATCTCAAGCCAGAAACATTATGTTTATAGCAAGATATT 516
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Qy 421 cccatccacacatcaagctgattgacttgctgtgtcgcacgaaatagaagaatgagtt 480
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Db 517 CCATTCCACACATCAAGCTGATTGACTTGTGCTGGCTCAGCAAAATAGAAATGAGATT 576
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Qy 481 gaattcaagaatatttttggagagccggaaattgtgtctcagaagaattgtgaactcag 540
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Db 577 GAATTTTAAAGAAATTTTGGAGCGCGGAATTTGTGCTCCAGAAATTTGAACCTACGAG 636
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Qy 541 cccctggtctgtagagctgcacgtgtgagagatagggctcatcaactacatcccttaagt 600
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Db 637 CCCCTGGTCTGAGGCTGACATGTGAGCATAGGCTCTCATCACTTACATCTCTTAAGT 686
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Qy 601 gggagcattcccttccctgtagagagacgaaagcaagaaacacatggcacaatcagtcag 660
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Db 697 GGAGCATCCCTTCTCTGGGAGACAGAACAGAAACACTGGCAAAATATCACAGCAGTG 726
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Qy 661 agttaagacttgtagaggaattcttcagcacaagagagagagctgtgccaagagcttatt 720
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Db 757 AGTTAGCACTTTATGATGAGGAATTTCTCAGCAGACGACGAGCTGGCAAGACTTTATT 816
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Qy 721 cgaagcttcgtgttaagagaccggaagcggctcacaatccaagaaggtctccagagac 780
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Db 817 CGGAACCTTGTGTTAAAGAGACCCGGAACGGCTCACAATCCAAGAGGCTCTCAGACAC 876
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Qy 781 cccttgatc 789
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Db 877 CCCTGGATC 885
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RESULT 3
BC022165 1883 bp mRNA linear ROD 28-JAN-2002
LOCUS Mus musculus, death-associated kinase 2, clone MGC:13742
DEFINITION IMAGE:4016911, mRNA, complete cds.
ACCESSION BC022165
VERSION BC022165.1 GI:18381096
KEYWORDS house mouse.
SOURCE MGC.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1883)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (25-JAN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
COMMENT Contact: MGC help desk

Email: cgabbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahy, Erin Helton, Mark Kettelman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whitting

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAK Plate: 18 Row: f Column: 7
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 6521216.

FEATURES
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/db_xref="taxon:10090"
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(clonal) outgrowth infected with the virus MMV."
/clone_lib="NCI-CGAP_Lu29"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
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NIPDPIKILIDELAIEDVGFKNIFQTPPEVAPEIYNDEPLGELADWMSIGVITY
ILISGASPLGDTKOETLANITAVSYDFEPEFSQSEIAKDFIRKLIVKERTKRLTI
OEALRHPIWITPVDTQOAMVRESVNVLEMEKQYVRRKMLSPSIVSLCNHLIRSLMK
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BASE COUNT 576 a 444 c 471 g 392 t
ORIGIN

Query Match 88.4%; Score 697.8; DB 10; Length 1883;
Best Local Similarity 92.8%; Pred. No. 9.2e-152;
Matches 732; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

Qy 1 tatgacatcgagagagctggtgagctgtgccaatcgatgaagaagtgcggag 60
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Db 157 TATGACATCGAGAGAGAGAGCTGGGACATGGCCAGTTTCATCGAAGAGTGGCGGAG 216
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Qy 61 aagagcaggggtgtgtagtgcagccaagtcatcaagaagcgagacggcgagc 120
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Db 217 AAGAGCACAGGCGTGTGATGACAGCCAAAGTTCTTAAAGAGAGCGAGCCGGCCAGC 276
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Qy 121 cggcggtgtgtgagccggagagagatcgagcggagaggttgaacatccctgcgaggtgtc 180
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Db 277 CGTCGGGGCTGTGCGCGGAGAGATGAGCGGAGGTGACATCTTCCGCGAGTCTG 336
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Qy 181 caccacaatgtcatcagctgcagcagcgtctatagagaccgacacgagcgtgtgtacatc 240
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Db 337 CACCCCAACATCATACAGCGTCTATGAGAACCGACCGACGAGTGTGCTCATC 396
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Qy 241 ctgagctagtgctgtagagagagccttcgattcctggtccgagagagtagcagat 300
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Db 397 CTGAGCTAGTGTCTGAGAGAGAGCTCTTGATTTCTGCTGCGCAGAAAGAGTCACTGAGT 456
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Qy 301 gagagagagccacagctcatcaatgaagcagatccctgtgaggttgaactcctcacaca 360
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Db 457 GAGGAGGAACACACACCTTCATTAAAGCAATCTGGATGGGTGAATTTACCTTCACACA 516
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Qy 361 aagaaatgtctcacttgatctcacaagccagaaacattgtttatagaagaagaatatt 420
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Db	517	AAGAAATTTGCTCATTGTGCATCTCAAGCCAGAAAACATCATGTTGTTAGACAAGAATATTC	576
Oy	421	cccatcccaacatacgaactgtaattgaccttggtcttggctcaagaatagaaatgtagtc	480
Db	577	CCCATTCCACACATCAAGCTGATTGACTTGGCCTGGCTCGTAAGAAATAGAAGATGGAGTT	636
Oy	481	gaattiaagaatatttttggagaccgcgaatttgttctccagaatatgtgaactacag	540
Db	637	GAAATTTAAAAACATTTTTTGGGACACCTGMAATTTTGTTGCTCCAGAAATCGTGAATAAGAC	696
Oy	541	ccccctgggtctggaagctcgatgcatgtlbgagcataagcgcltcatacctaacttcctaagt	600
Db	697	CCACGTGAGCATGTGAGGCCGACATGTGGAGCTATTGGAGATCATCACCTTCATCTTCTAAGT	756
Oy	601	ggagcatccccttctccctgtyggagagacaacgaagaagaagaacacatcgsgaaatatacactgagt	660
Db	757	GGAGGCTTCCCCCTTCCTGCTGGGAGACACAAACAAAGAACCCCTGGCAAAATATACACTGCTGTG	816
Oy	661	agttacgactcttgatlgagaattcttccagccatacagcgagctcgycggccaagacttatlt	720
Db	817	AGTTACGACTTTGATGAGAGAAATCTTTCAGCCACGACAAGCGAGTGTGGCCAAGACTTCATT	876
Oy	721	cggaaagctcttggttaaagaagaccgccgaagaacggctcacaatccaaaggaccttaagacat	780
Db	877	CGGAAGCTTCTTGTGTGAAGAGACCOCGGAAGCGCTTACCATTCACAAGAGGCTTCAGACAT	936
Oy	781	cccttgagtc	789
Db	937	CCCTGGATC	945
RESULT	4		
ABO18002		1757 bp	mRNA linear ROD 04-DEC-1999
LOCUS			
DEFINITION	Mus musculus mRNA for Death-associated protein kinase 2, complete cds.		
ACCESSION	ABO18002		
VERSION	ABO18002.1 GI:6521216		
KEYWORDS	Death-associated protein kinase 2.		
SOURCE	Mus musculus cDNA to mRNA.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	Kawai,T., Nomura,F., Hoshino,K., Copeland,N.G., Gilbert,D.J., Jenkins,N.A. and Akira,S.		
TITLE	Death-associated protein kinase 2 is a new calcium/calmodulin-dependent protein kinase that signals apoptosis through its catalytic activity		
JOURNAL MEDLINE	Oncogene 18 (23), 3471-3480 (1999)		
REFERENCE	99303018		
AUTHORS	2 (bases 1 to 1757)		
TITLE	Akira,S. and Kawai,T.		
JOURNAL	Direct Submission		
FEATURES	Submitted (28-SEP-1998) Shizu Akira, Hyogo College of Medicine, Department of Biochemistry; Mukogawa-cho 1-1, Nishinomiya, Hyogo 663-8501, Japan (E-mail:akira@hyo-med.ac.jp, Tel:81-798-45-6357, Fax:81-798-46-3164)		
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	/db_xref="gi:6521217"		
	/translation="MYQASMPSPNMEPKOOKVDFVDYDGELSGOPAIYKKCREKS		
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Query Match	Best Local Similarity	Score	DB	Length
Matches 729; Conservative	92.48;	Pred. No. 1.2e-150;	Mismatches 60; Indels 0; Gaps 0;	
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BASE COUNT	438 a	443 c	487 g	389 t
ORIGIN				
QY	1	tatgacatcgagaggaagctgggaggtgagccagtttgcacatcgttgaagaagtgcgagag	60	
DB	178	TATGACATCGAGAGAGAGACTGGCGAGTGGCCAGTTGGCATCGTAAAGAAGCGCGGAG	237	
QY	61	aagagcaggggcttgagtatgcagcaagttcatcaagaagcggcagagccggcgagc	120	
DB	238	AAGAGCAGGGGCTTGAGTATGCAAGCCAAAGTTCAATTAAGAAGAGCAAGCGGGCCAGC	297	
QY	121	cggcgcggttgtagccggagagagatcgagcgagaggttgagcatcctgcgaggtgctg	180	
DB	298	CGTCGGGCGTGTGCGGGAGGAATCCAGCGGAGGTGAGCATCTCGCGAGGTGCTG	357	
QY	181	caccacaatgtaatcagcgtgcacgagtcataagaaaccgacccgacgttgtagcacat	240	
DB	358	CACCCCAATCATCATCACCTGCAGGACGCTCTATGAAACCGCACCGACGTGCTCATC	417	
QY	241	cttgagctagtggtcggagagagcttcgtacattccggcccgagaagaagtcactgagt	300	
DB	418	CTTGAGCTAGTGTCCGGAGAGAACTGTTTGATTTCTCGGCCCAAGAGAGTCGTTAAGT	477	
QY	301	gagagagagggcacaacagttcataaagaagatcctgtagtgagggtgaactacccaaca	360	
DB	478	GAGGAGGAAGCCACACGAGCTTCATTAAGCAGATCTCGATGGGAGTAATTAACCTCACACA	537	
QY	361	aagaaatgtgcactttgatactcaagccagaaacatattgttttagacaagaatactt	420	
DB	538	AAGAAATGTGCACCTTGATGATCAAGCCAGAAACATCATGTGTTAGACAAAGATATC	597	
QY	421	cccatccacaatcaagctgattgactttgcttgctcagcaagaaatagaagatgaggt	480	
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QY	481	gaatttaagaataatttttgggagcccggaatttgttgcacgaaatgttgactcagag	540	
DB	658	GAAATTTAAAMAAATTTTGGGACACCTGAAATTTGGCGTCCGAAATGATGAACTATGAG	717	
QY	541	ccccggggtctgagagctacagtcggaacatagagcgatcatcaccttacccttaagt	600	
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QY	601	ggaagatcccttcccttgaggagacaagacgagaaacacttggcacaatactacatagtg	660	
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QY	661	agttgacttgatagagaattcttcagcaatacagagagagcttggccaagaacttatt	720	
DB	838	AGTTAGACTTTGATGAGGAATTTCTTACGCCAGACAAAGGAGACTGGCCAAAGACTTCAT	897	
QY	721	cgaagacttctgtttaaagagaccggaaacggctcacaaatccaaaggctctagagac	780	
DB	898	CGGAACCTCTGTGTAAGAAGACCCGGAACGGCTTAACATCCAAAGAGCTCTCAGACAT	957	
QY	781	ccctggatc	789	
DB	958	CCCTGGATC	966	

LOCUS AF052942 1474 bp mRNA linear ROD 20-JAN-2000
 DEFINITION Mus musculus DAP-kinase related protein 1 mRNA, partial cds.
 ACCESSION AF052942
 VERSION AF052942.1 GI:3560544
 KEYWORDS house mouse.
 SOURCE Mus musculus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 1474)
 AUTHORS Inbal, B., Shani, G., Cohen, O., Kissil, J. L. and Kimchi, A.
 TITLE Death-associated protein kinase-related protein 1, a novel serine/threonine kinase involved in apoptosis
 JOURNAL Mol. Cell. Biol. 20 (3), 1044-1054 (2000)
 MEDLINE 20094983
 PUBMED 10629061
 REFERENCE 2 (bases 1 to 1474)
 AUTHORS Kimchi, A. and Inbal, B.
 TITLE Direct Submission
 JOURNAL Submitted (09-MAR-1998) Molecular Genetics, Weizmann Institute of Science, Rehovot 76100, Israel
 FEATURES
 source Location/Qualifiers
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 /db_xref="taxon:10090"
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 FDLQAHELSSEBATSFIQILDGVNLTAKIAHDLKPEINMLDKNIPPHIL
 IDFLAHEIDGVEFKNIGTPEFVAVETIYPLGLDAMWSIGVTYLLSGASP
 LGDTKQETLANIYAVSYDEFEFSQSELAKEIRKLTLVKEPRKRLTIDELRHPI
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 LRNCESTEENIARRKALHRRRSSTS"
 BASE COUNT 399 a 356 c 371 g 348 t
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 Best Local Similarity 91.8%; Pred. No. 5.5e-122;
 Matches 602; Conservative 0; Mismatches 54; Indels 0; Gaps 0;
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 Oy 194 tcaagcgcgaagcagctcatgagaaacgcagcagcgtgtgacacatcttgagctagt 253
 Db 61 TCACGAGGACGACGCTCTATGAAACGACGACGCTGCTCATCTTGAAGTACGAGCA 120
 Oy 254 ctgagagagagcctctgattctctgcgcgaggaagctcattgagtgaggagagcca 313
 Db 121 CCGGAGGAGAACTGTTGATTCTCTGGCCCGAAGAGACTCTTAAAGTACGAGCA 180
 Oy 314 ccagcctcatatgaacagatcctgagtgagggtacactcaccacaagaanaattgtctc 373
 Db 181 CCAGCTTCATTAAACAGATCTCTGATGGGTGAATTAACCTTACACAAAGAAATTTGCTC 240
 Oy 374 acttggatctcaagccagaaacattatgtctgtagacaagaataatcccatccacaca 433
 Db 241 ACTTTGATCTCAACCCAGAAACATCATGTTGTAGACAAAGATATCCCAATTTCCACACA 300
 Oy 434 tcaagcgcattgactctgtctgcgcagaaatagaaagagtgagggttgaaatagaata 493
 Db 301 TCAGAGCTGATGACTTTTGCTGGCTGCAGAAATAGAAAGATGAGATTGAATTTAAAAACA 360
 Oy 494 tttttggagcgcggaattgtgtctccagaatgtgaaactagagagcccttggtctg 553
 Db 361 TTTTGGACACCTGAATTTGTGCTCCAGAAATCGTAATGAGGCACTGGGACTGG 420

Oy 554 agcgtgacatgtgagacatagagcgtcatcacatcctcttaagtggagcattccctt 613
 Db 421 AGCGGACATGTGGAGCATGTGGAGCATACCTATATCTTCTTAAGTGGAGCTGCCCT 480
 Oy 614 tccctggagacagaaagaaacacgcgcgaatatacatcagtgagtgactgttg 673
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 Oy 674 atgaggaattcttcagcatcagagcagcgtgcgcgaagacttaattcggaagctctg 733
 Db 541 ATGAGGAATTTCTTACGACGACAGCGAGCGCCCAAGACTTCAATTCGGAAGCTTCTG 600
 Oy 734 ttaagagaccgcggaagcgtctcaacatccaagagcctgaagaccctggatc 789
 Db 601 TGAAGAACCAACGGAACGCGCTTACCATTCAGAGAGCTCTCAGACATCTCTGATC 656
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 AB022341 2055 bp mRNA linear PRI 24-JUN-1999
 LOCUS AB022341
 DEFINITION Homo sapiens mRNA for ZIP kinase, complete cds.
 ACCESSION AB022341
 VERSION AB022341.1 GI:5162883
 KEYWORDS ZIP kinase.
 SOURCE Homo sapiens cell_line:Hela RCB0007 CDNA to mRNA, clone_lib:Hela cell CDNA library.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (sites)
 AUTHORS Murata-Hori, M., Suizu, F., Iwasaki, T., Kikuchi, A. and Hosoya, H.
 TITLE ZIP kinase identified as a novel myosin regulatory light chain kinase in HeLa cells
 JOURNAL FEBS Lett. 451 (1), 81-84 (1999)
 MEDLINE 99283879
 REFERENCE 2 (bases 1 to 2055)
 AUTHORS Iwasaki, T., Murata-Hori, M. and Hosoya, H.
 TITLE Direct Submission
 JOURNAL Submitted (12-JAN-1999) Takahiro Iwasaki, Hiroshima University, Department of Biological Science, 1-3-1 Kagamiyama, Higashi-Hiroshima, Hiroshima 739-8526, Japan
 (E-mail:u0775006@ipc.hiroshima-u.ac.jp, Tel:81-824-7443(ex.7443), Fax:81-824-0734)
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 2055
 /note="24 a nucleotides"
 BASE COUNT 393 a 618 c 726 g 318 t
 ORIGIN
 polyA_site

Db 526 GAGTTCAGAACATCTTTGGCACACCCGAGTTGTGCCCCCGAGATCGTAGACTATGAG 585
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Db 586 CCACTTGCGCTTGAGAGCTGACATGTGAGCATTTGGCTCATCACTACATCTCTTGAGC 645
QY 601 ggaacatccctctcccttgagagacagaaagcaaaacttggcaaatatcacatcaatg 660
Db 646 GAGAGCTCCCATCTCTGGCGGAGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 705
QY 661 agttaagacttgaatgaagaattctcaagcatalcagagcagcttggccaagaacttatt 720
Db 706 AACTATGACTTTGATGAGAAATCTACAGACAGCAGAGCTGGCCAAAGAGACTTCATC 765
QY 721 cggaaagctcttggttaagaagaccggaagcgtcaacaatccaagaagctctcagaac 780
Db 766 CGAGAGCTGCTGTGTCAAAGACCCCAAGAGAGAGATGCATCCGACAGAGCTTGAGCAT 825
QY 781 cccttgatc 789
Db 826 TCCTGGATC 834

RESULT 8
AR076190
LOCUS AR076190 1429 bp DNA linear PAT 30-AUG-2000
DEFINITION Sequence 4 from patent US 5958748.
ACCESSION AR076190
VERSION AR076190.1 GI:10002936
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1429)
AUTHORS Akira,S. and Kawai,T.
TITLE DNA coding for serine/threonine kinase
JOURNAL Patent: US 5958748-A 4 28-SEP-1999;
FEATURES
source 1..1429
/organism="unknown"
BASE COUNT 309 a 425 c 475 g 220 t
ORIGIN

Query Match 62.7%; Score 494.6; DB 6; Length 1429;
Best Local Similarity 76.7%; Pred. No. 1.5e-104;
Matches 605; Conservative 0; Mismatches 184; Indels 0; Gaps 0;

QY 1 tatgacatcgagagagagctgggagtgagcagtttgccatcgctgaagaagtccggag 60
Db 46 TATGACATGGAGAGAGAGCTTGCCAGTGGCCATTTGGCTCGTCCGCAAGTCCAGCAG 105
QY 61 aagaagcaggggcttgagtaagcaaaagttcatcaagaagcggcagagcggcgagc 120
Db 106 AAGGCGACGGGCGATGAGTATGACGCCAAGTTCATCAAGAGGCGGCGCCATCCAGC 165
QY 121 cggcgcggtgtgagccgggagagatcgagcgggaggttgagcatccttcggcgagtgctg 180
Db 166 CGGCGGCGTGTGAGCGGCGGAGATCGAAGCGGAGGTGAGCATCTGCGCCGAGATCCGC 225
QY 181 caccacaatgtcatcaacgcgcagcagctctatagaaaccgcagcagcgtgtgacatc 240
Db 226 CACCCCAACATCATACACCTGATGACGTCTTGAGAGAACAGACAGATGTGCTGATC 285
QY 241 cttagcctagtgctcggagagagacttccatcccttggccagaagaagtagtactag 300
Db 286 CTGAGACTGCTGTCCGCTGCGAGCTTTTGACTTCCTGCGCAGAAAGAGTCAATTGACG 345
QY 301 gaggagagagccacacagctcatatagcagaatcccttgagtggttgaaactaccctcaaca 360
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QY 361 aagaataatgtcacttgaatcccaagccagaatacatatgtgttagcaagaatatt 420

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QY 421 cccattccacacatcaagctgattgacttgtcttgctcaagaatagaatagatgagtt 480
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Db 586 CCACTTGCGCTTGAGAGCTGACATGTGAGCATTTGGCTCATCACTACATCTCTTGAGC 645
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Db 646 GAGAGCTCCCATCTCTGGCGGAGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 705
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Db 706 AACTATGACTTTGATGAGAAATCTACAGACAGCAGAGCTGGCCAAAGAGACTTCATC 765
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QY 781 cccttgatc 789
Db 826 TCCTGGATC 834

RESULT 9
AR124103
LOCUS AR124103 1429 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 4 from patent US 6171841.
ACCESSION AR124103
VERSION AR124103.1 GI:14109464
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1429)
AUTHORS Akira,S. and Kawai,T.
TITLE DNA coding for serine/threonine kinase
JOURNAL Patent: US 6171841-A 4 09-JAN-2001;
FEATURES
source 1..1429
/organism="unknown"
BASE COUNT 309 a 425 c 475 g 220 t
ORIGIN

Query Match 62.7%; Score 494.6; DB 6; Length 1429;
Best Local Similarity 76.7%; Pred. No. 1.5e-104;
Matches 605; Conservative 0; Mismatches 184; Indels 0; Gaps 0;

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Db 106 AAGGCGACGGGCGATGAGTATGACGCCAAGTTCATCAAGAGGCGGCGCCATCCAGC 165
QY 121 cggcgcggtgtgagccgggagagatcgagcgggaggttgagcatccttcggcgagtgctg 180
Db 166 CGGCGGCGTGTGAGCGGCGGAGATCGAAGCGGAGGTGAGCATCTGCGCCGAGATCCGC 225
QY 181 caccacaatgtcatcaacgcgcagcagctctatagaaaccgcagcagcgtgtgtgacatc 240
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QY	241	cttagctagctagctgctgagagagagcttctgattctctgcccgaagagagctcaagtc	300
Db	286	CTGAGGCTGGGTGTCGGGAGGAGCTTTTGACTTCTTGCCGAGAAAGATCACTTTACG	345
QY	301	gaggagagagccacacgaactcattcaagacagatccctggatgggtgnaacitccctcacaca	360
Db	346	GAGATGAGGGCCACGACAGTTCTCCTCAAAACAAATCCTAACAGGTGTCCTACTCTGCATCC	405
QY	361	aagaaattgtcactcttgatctcaagccagaaaaaatltgltgttagcaaaaatatt	420
Db	406	AAGGCATCCGACACTTTGACCTGAAGCCGAGAAACATCATGTTGCTGGAGAACACACGCA	465
QY	421	cccatccacacatcaagaactgattgacttgctgtgctcacaagaatagaagatcgagtt	480
Db	466	GCCACGCCCCCGCATTTAAGCTCATGACTTGTGGCATTCGGGACACAGAGATCGAGCTGGCAGC	525
QY	481	gaatttaagaatatttttggagacgcgggaatttltgtctccagaatattgttaactaagag	540
Db	526	GAGTTCAAGAACATCTTTGGCACACCCGAGTTTGTGCGCCCCGAGATCGTAACCTATGAG	585
QY	541	ccccgggtctggagagctcgacatgtggagacataagcgtcatcacactacatcctttaagt	600
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QY	601	ggagacatcccccttctcgtggagagacagaaagaaacactggcacaatatcatctcaagt	660
Db	646	GGAGGCTCCCCATTCCTCTGGGGAGACCCAGACAGGAGAGCGCTGACCAACATCTCAGCACTG	705
QY	661	agttcgcacttggatgaggaatctctcaagccataagcagagctggtggcagaagacttaatt	720
Db	706	AACCTATGACTTTGATGAGAGAACTACTTCAAGCACACACGACGAGCTGGCCAAAGACTTATTC	765
QY	721	cggaaagctctctggttaaaagagacccggaaacggtctacataccaaagagctctcagacac	780
Db	766	CCGAGGCTGCTGCTGCTCAAGACCCCAAGAGAGAGATGACATCTGCACAGAGCTTGAGCAT	825
QY	781	cccttgatc 789	
Db	826	TCTGTGATC 834	
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LOCUS	E23385		
DEFINITION	DNA encoding serine/threonine kinase.		
ACCESSION	E23385		
VERSION	E23385.1 GI:13024387		
KEYWORDS	JP 1999098984-A/2.		
SOURCE	unidentified.		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 1429)		
AUTHORS	Shizuo,S.T.K.K.		
TITLE	DNA encoding serine/threonine kinase		
JOURNAL	Patent: JP 1999098984-A 2 13-APR-1999;		
COMMENT	SCIENCE & TECH AGENCY		
OS	Unidentified		
PN	JP 1999098984-A/2		
PD	13-APR-1999		
PR	26-SEP-1997 JP 1997261589		
PI	SHIZUO SHINRA,TARO KAWAI		
PC	C12N1/09,C12N1/21,C12N9/12//((C12N1/09,C12R1:91),(C12N1/21,		
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Strandness:	Double;		
CC	Topology: Linear;		
FH	Key	Location/Qualifiers	
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Best Local Similarity	76.7%	Pred. No. 1.5e-104;			
Matches 605; Conservative	0;	Mismatches 184;	Indels 0;	Gaps 0;	
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Qy	61	aagagcagggccttgagatgcatgacccaatgtctaaagaagcggcagagccggcgagc	120		
Db	106	AAGGCGACGGGCATGAGATATGACGCCAAGTTCATCAAGAGCGGGCCCTGCCATCCAGC	165		
Qy	121	cggcgcggtgagccggaagagatcagacgggaggttgagcatccttcgycgaggtgctg	180		
Db	166	CGGCGCGGTGTGAGCGGGGAGAGATGCAAGCGCGAGGTGAGCATCTCGCGAGATCGCG	225		
Qy	181	cacacaatgtcatcagctgcaagagctcctaagaagacgcacggcggtgtgcatcatc	240		
Db	226	CACCCCAACATCATATACCTGCATGACCTGTTCAGAAACAAGACAGATGTGTCTGATC	285		
Qy	241	cttgagctagtgctctggaagagagctcttcgattcctctgcccagaaagagtcactgag	300		
Db	286	CTGGAGCTGTGTCCGGTGGGAGGCTTTTCGACTTCCTCGGCCGAGGAAGATCATTTGACG	345		
Qy	301	gagagagagccacacagcttcaatgaagacagatcctgtagtgggtggaactaacttcacac	360		
Db	346	GAGGATGAGGCGCACCGAGTTCCTCAACAAATCTTACAGGGGTGTCCACTTACTCTACCTCC	405		
Qy	361	aagaaatgtgcatttgatctcaagccgaaaaacatactgtgttgagacaagaatat	420		
Db	406	AAGCCGATGCGACACTTTGACTGAGGCCCGAAGACATCATGTGTGTGGACAGACAGCA	465		
Qy	421	cccatccacacatcaagctgattgacttggcttgctcagcaatagaagaatgaggtc	480		
Db	466	GCGAGCGCCCGCATTAAGCTCATGCACTTTGGCATCGCGCACAGGATCGAGGCTTGGCAGC	525		
Qy	481	gaattaaagaatatltttgggagccgggaatttgttgcagaagaattgaaactagag	540		
Db	526	GAGTTCAAAACATCTTTGGCACACCCGAGTTTGTGCCCCCGAGATGTGTCAACTATAG	585		
Qy	541	ccccctggtcgtgaggtctacacatgagagcatagagcgatcatcactatcctcttaagt	600		
Db	586	CCACTTGGCTTGAGAGGCTACATGTGAGACATTTGGCGTACATCACTCACTCCTCGAGC	645		
Qy	601	gagagcatcccttccctctgtagagacagaaagcaaacctgtgcaaatatacaatcaagt	660		
Db	646	GGAGCGTCCCATTCCTCTGGCGAGACCAAGAGAGACGCTGTACCAACCTTCTCACAGTG	705		
Qy	661	agtagactttgataagaatctctcagcacaacagagagagctgagcaagacttatt	720		
Db	706	AACATAAGACTTTGATATAGAAATACCTTCACACACACAGGAGACTGTGCCAAGGACTTCATC	765		
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Db	766	CGGAGCGTGTGTCAAAAGACCCCAAGAGAGAGATGACCATCGCACAGAGCTTGAGGAT	825		
Qy	781	cccttgagtc 789			
Db	826	TCCTTGATC 834			
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LOCUS	AB007144				
DEFINITION	Homo sapiens mRNA for ZIP-Kinase, complete cds.				
ACCESSION	AB007144				
VERSION	AB007144.1	GI:2911155			
KEYWORDS	ZIP-Kinase.				
SOURCE	Homo sapiens	CDNA	to mRNA.		

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 2105)
AUTHORS Akira, S. and Kawai, T.
TITLE Direct Substitution
JOURNAL Submitted (10-SEP-1997) Shizuoka Akira, Hyogo College of Medicine,
Department of Biochemistry, Mukogawa-cho 1-1, Nishinomiya, Hyogo
663, Japan (E-mail: akira@hyo-med.ac.jp, Tel: +81-798-45-6357,
Fax: +81-798-46-3164)
2 (sites)
REFERENCE Kawai, T., Matsumoto, M., Takeda, K., Sanjo, H. and Akira, S.
AUTHORS ZIP kinase, a novel serine/threonine kinase which mediates
TITLE apoptosis
JOURNAL Mol. Cell. Biol. 18 (3), 1642-1651 (1998)
FEATURES
source location/Qualifiers
1..2105
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Best Local Similarity 76.6%; Pred. No. 2.7e-104;
Matches 604; Conservative 0; Mismatches 184; Indels 0; Gaps 0;
QY 1 tatgaacatcgaaagagagcgaggagtgccattgcccctgctgaagaagtcggggag 60
DB 130 TATGAGATGGGGAGGAGGAGCTGGGACGCGCACTTGGCATGCGGAAGTGGCCGAC 189
QY aagagcagcgaggcttgagtaatgcaagtcatacaagaagcgagcgaggagc 120
DB 190 AAGGCGACGGGCAAGGAGTACGACCAAGTTCATCAAGAGCGCCCGCTGTATCCAGC 249
QY 121 cggcgcggtgtgagcgaggagatcgagcgagggtgagcaatcctcgcgagtgctg 180
DB 250 CGCGGTGGGTGAGCGGAGGAGATCGAGCGGAGGTGAACATCTCGCGGAGATCCG 309
QY 181 caccacaatgtcatcagcgtcgacagagctctatagagaacgcagcagcgatggtgcaatc 240
DB 310 CACCCCAACATCATCAACCTCGACGACATCTTGAGAGAAAGACGGACGTGGTCTCATC 369
QY 241 ctgagactagtgctgagagagagccttcgattcccttgccagagagagtgactagat 300
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QY 781 cccctgagat 788
DB 910 TCCTGGAT 917
RESULT 12
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LOCUS Sequence 3 from patent US 5958748.
DEFINITION AR076189
ACCESSION AR076189 GI:10002935
VERSION AR076189.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2132)
AUTHORS Akira, S. and Kawai, T.
TITLE DNA coding for serine/threonine kinase
JOURNAL Patent: US 5958748-A 3 28-SEP-1999;
FEATURES location/Qualifiers
source 1..2132
BASE COUNT 429 a 630 c 741 g 332 t
ORIGIN
Query Match 62.6%; Score 493.6; DB 6; Length 2132;
Best Local Similarity 76.6%; Pred. No. 2.7e-104;
Matches 604; Conservative 0; Mismatches 184; Indels 0; Gaps 0;
QY 1 tatgaacatcgaaagagagcgaggagtgccattgcccctgctgaagaagtcggggag 60
DB 130 TATGAGATGGGGAGGAGGAGCTGGGACGCGCACTTGGCATGCGGAAGTGGCCGAC 189
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QY 181 caccacaatgtcatcagcgtcgacagagctctatagagaacgcagcagcgatggtgcaatc 240
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QY 241 ctgagactagtgctgagagagagcttcgattcccttgccagagagagtgactagat 300
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QY 481 gaatttaagaatatatttggagagccggaatttggctccagaataatgtgaactaagag 540
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DB 850 CGCGGCTGCTGCTCAAAAGATCCCAAGCGGAGATGACATTGCCCAAGAGCTGGAACAT 909
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DB 910 TCCTGGAT 917
RESULT 13
AR124102 2132 bp DNA linear PAT 16-MAY-2001
LOCUS AR124102
DEFINITION Sequence 3 from patent US 6171841.
ACCESSION AR124102
VERSION AR124102.1 GI:14109463
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2132)
AUTHORS Akira, S. and Kawai, T.
TITLE DNA coding for serine/threonine kinase
JOURNAL Patent: US 6171841-A 3 09-JAN-2001;
FEATURES
source 1. 2132
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BASE COUNT 429 a 630 c 741 g 332 t
ORIGIN
Query Match 62.6%; Score 493.6; DB 6; Length 2132;
Best Local Similarity 76.6%; Pred. No. 2,7e-104;
Matches 604; Conservative 0; Mismatches 184; Indels 0; Gaps 0;

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DB 370 CTGAGACTGGTCTCTGGGGGAGCTTGTGACTTCGCGGAGAAAGATGCTGACG 429
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DB 910 TCCTGGAT 917
RESULT 14
E23384 2132 bp DNA linear PAT 07-FEB-2001
LOCUS E23384
DEFINITION DNA encoding serine/threonine kinase.
ACCESSION E23384
VERSION E23384.1 GI:13024386
KEYWORDS JP 199098984-A/1.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2132)
AUTHORS Shizuo, S. T. K. K.
TITLE DNA encoding serine/threonine kinase
JOURNAL Patent: JP 199098984-A 1 13-APR-1999;
COMMENT
OS Unidentified
PN JP 199098984-A/1
PD 13-APR-1999
PE 26-SEP-1997 JP 1997261589
PR
PI SHIZUO SHINRA, TARO KAWAI
PC C12N15/09, C12N1/21, C12N9/12, C12N15/00, C12N1/91, C12N1/21,
PC C12N1/19,
PC C12N9/12, C12N1/19, C12N15/00, C12N15/00, C12N1/91 CC
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CC Topology: Linear;
FH key Location/Qualifiers


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QY 481 gaattagaatatttggagcgcggaattgtgtccagaattgtgaactagag 540
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Db 851 GGTGCATCCCGTCTCTGGGCGAGACCAAGCAGAGAGCGCTACCCACATCTCAGCCGTG 910
QY 661 agtiacgaacttgaagaatctctcagccatacagagcagctggccaaggacttalt 720
Db 911 AACTACGACTTCGACGAGAGACTACTTCAGCAACACCGCGAGCTGGCCAAAGACTTCATT 970
QY 721 cggaaagcttctgtttaaagaagaccggaacggtcacaatccaagaggtctcagacac 780
Db 971 CGCCGGCTGCTGTCAAAGATCCCAAGCGAGAAATGACCATTTGCCAGAGCCTGGAACAT 1030
QY 781 ccctggat 788
Db 1031 TCCTGGAT 1038
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